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RAW SEQUENCE LISTING

DATE: 08/28/2001

PATENT APPLICATION: US/09/752,514

TIME: 11:51:18

Input Set : A:\KLINEFELTER1C.txt

Output Set: N:\CRF3\08282001\I752514.raw

3 <110> APPLICANT: KLINEFELTER, Gary  
5 <120> TITLE OF INVENTION: METHOD FOR EVALUATING AND AFFECTING MALE FERTILITY  
7 <130> FILE REFERENCE: KLINEFELTER=1C  
9 <140> CURRENT APPLICATION NUMBER: 09/752,514  
10 <141> CURRENT FILING DATE: 2001-01-03  
12 <150> PRIOR APPLICATION NUMBER: US 09/123,492  
13 <151> PRIOR FILING DATE: 1998-07-28  
15 <150> PRIOR APPLICATION NUMBER: PCT/US97/01725  
16 <151> PRIOR FILING DATE: 1998-01-29  
18 <150> PRIOR APPLICATION NUMBER: US 08/593,677  
19 <151> PRIOR FILING DATE: 1996-01-29  
21 <150> PRIOR APPLICATION NUMBER: US 60/082,753  
22 <151> PRIOR FILING DATE: 1998-04-23  
24 <160> NUMBER OF SEQ ID NOS: 4  
26 <170> SOFTWARE: PatentIn version 3.1  
28 <210> SEQ ID NO: 1  
29 <211> LENGTH: 189  
30 <212> TYPE: PRT  
31 <213> ORGANISM: Homo sapiens  
33 <400> SEQUENCE: 1  
35 Met Ala Ser Lys Arg Ala Leu Val Ile Leu Ala Lys Gly Ala Glu Glu  
36 1 5 10 15  
39 Met Glu Thr Val Ile Pro Val Asp Val Met Arg Arg Ala Gly Ile Lys  
40 20 25 30  
43 Val Thr Val Ala Gly Leu Ala Gly Lys Asp Pro Val Gln Cys Ser Arg  
44 35 40 45  
47 Asp Val Val Ile Cys Pro Asp Ala Ser Leu Glu Asp Ala Lys Lys Glu  
48 50 55 60  
51 Gly Pro Tyr Asp Val Val Val Leu Pro Gly Gly Asn Leu Gly Ala Gln  
52 65 70 75 80  
55 Asn Leu Ser Glu Ser Ala Ala Val Lys Glu Ile Leu Lys Glu Gln Glu  
56 85 90 95  
59 Asn Arg Lys Gly Leu Ile Ala Ala Ile Cys Ala Gly Pro Thr Ala Leu  
60 100 105 110  
63 Leu Ala His Glu Ile Gly Cys Gly Ser Lys Val Thr Thr His Pro Leu  
64 115 120 125  
67 Ala Lys Asp Lys Met Met Asn Gly Gly His Tyr Thr Tyr Ser Glu Asn  
68 130 135 140  
71 Arg Val Glu Lys Asp Gly Leu Ile Leu Thr Ser Arg Gly Pro Gly Thr  
72 145 150 155 160  
75 Ser Phe Glu Phe Ala Leu Ala Ile Val Glu Ala Leu Asn Gly Lys Glu  
76 165 170 175  
79 Val Ala Ala Gln Val Lys Ala Pro Leu Val Leu Lys Asp  
80 180 185  
83 <210> SEQ ID NO: 2  
84 <211> LENGTH: 980  
85 <212> TYPE: DNA

ENTERED

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86 <213> ORGANISM: Rattus rattus
88 <220> FEATURE:
89 <221> NAME/KEY: CDS
90 <222> LOCATION: (190)..(756)
91 <223> OTHER INFORMATION:
94 <400> SEQUENCE: 2
95 gctgtgcaga gccgtctggc agggttgacc tcctaaaggg atattccatc tttattaatc      60
97 attagtagtg tggtcagaga cttagcacca ttggtctccc ccaacctggg ccagacattt      120
99 cagcagttta tcggaacagc aacaacagca acaaaacctt caaaattttac aagtctttaa      180
101 gaaatagaaa atg gca tcc aaa aga gct ctg gtc atc cta gcc aaa gga gca      231
102      Met Ala Ser Lys Arg Ala Leu Val Ile Leu Ala Lys Gly Ala
103      1          5          10
105 gag gag atg gag aca gtg att cct gtg gac atc atg cgg cga gct ggg      279
106 Glu Glu Met Glu Thr Val Ile Pro Val Asp Ile Met Arg Arg Ala Gly
107 15          20          25          30
109 att aaa gtc acc gtt gca ggc ttg gct ggg aag gac ccc gtg cag tgt      327
110 Ile Lys Val Thr Val Ala Gly Leu Ala Gly Lys Asp Pro Val Gln Cys
111      35          40          45
113 agc cgt gat gta gtg att tgt ccg gat acc agt ctg gaa gaa gca aaa      375
114 Ser Arg Asp Val Val Ile Cys Pro Asp Thr Ser Leu Glu Glu Ala Lys
115      50          55          60
117 aca cag gga cca tac gat gtg gtt gtt ctt cca gga gga aat ctg ggt      423
118 Thr Gln Gly Pro Tyr Asp Val Val Val Leu Pro Gly Gly Asn Leu Gly
119      65          70          75
121 gca cag aac tta tct gag tcg gct ttg gtg aag gag atc ctc aag gag      471
122 Ala Gln Asn Leu Ser Glu Ser Ala Leu Val Lys Glu Ile Leu Lys Glu
123      80          85          90
125 cag gag aac agg aag ggc ctc ata gct gcc atc tgt gcg ggt cct acg      519
126 Gln Glu Asn Arg Lys Gly Leu Ile Ala Ala Ile Cys Ala Gly Pro Thr
127 95          100          105          110
129 gcc ctg ctg gct cac gaa gta ggc ttt gga tgc aag gtt aca tcg cac      567
130 Ala Leu Leu Ala His Glu Val Gly Phe Gly Cys Lys Val Thr Ser His
131      115          120          125
133 cca ttg gct aag gac aaa atg atg aac ggc agt cac tac agc tac tca      615
134 Pro Leu Ala Lys Asp Lys Met Met Asn Gly Ser His Tyr Ser Tyr Ser
135      130          135          140
137 gag agc cgt gtg gag aag gac ggc ctc atc ctc acc agc cgt ggg cct      663
138 Glu Ser Arg Val Glu Lys Asp Gly Leu Ile Leu Thr Ser Arg Gly Pro
139      145          150          155
141 ggg acc agc ttc gag ttt gcg ctg gcc att gtg gag gca ctc agt ggc      711
142 Gly Thr Ser Phe Glu Phe Ala Leu Ala Ile Val Glu Ala Leu Ser Gly
143      160          165          170
145 aag gac atg gct aac caa gtg aag gcc ccg ctt gtt ctc aaa gac      756
146 Lys Asp Met Ala Asn Gln Val Lys Ala Pro Leu Val Leu Lys Asp
147 175          180          185
149 tagagagccc aagccctgga ccttggaacc ccaggctgag caggcattgg aagcccacta      816
151 gtgtgtccac agcccagtga acctggcatt ggaagcccac tagtgtgtcc acagcccagt      876
153 gaacctcagg aactaacgtg tgaagtagcc cgctgctcag gaatctcgcc ctggctctgt      936
155 actattctga gccttgctag tagaataaac agttcccaa gctc      980

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158 <210> SEQ ID NO: 3
159 <211> LENGTH: 189
160 <212> TYPE: PRT
161 <213> ORGANISM: Rattus rattus
163 <400> SEQUENCE: 3
165 Met Ala Ser Lys Arg Ala Leu Val Ile Leu Ala Lys Gly Ala Glu Glu
166 1 5 10 15
169 Met Glu Thr Val Ile Pro Val Asp Ile Met Arg Arg Ala Gly Ile Lys
170 20 25 30
173 Val Thr Val Ala Gly Leu Ala Gly Lys Asp Pro Val Gln Cys Ser Arg
174 35 40 45
177 Asp Val Val Ile Cys Pro Asp Thr Ser Leu Glu Glu Ala Lys Thr Gln
178 50 55 60
181 Gly Pro Tyr Asp Val Val Leu Pro Gly Gly Asn Leu Gly Ala Gln
182 65 70 75 80
185 Asn Leu Ser Glu Ser Ala Leu Val Lys Glu Ile Leu Lys Glu Gln Glu
186 85 90 95
189 Asn Arg Lys Gly Leu Ile Ala Ala Ile Cys Ala Gly Pro Thr Ala Leu
190 100 105 110
193 Leu Ala His Glu Val Gly Phe Gly Cys Lys Val Thr Ser His Pro Leu
194 115 120 125
197 Ala Lys Asp Lys Met Met Asn Gly Ser His Tyr Ser Tyr Ser Glu Ser
198 130 135 140
201 Arg Val Glu Lys Asp Gly Leu Ile Leu Thr Ser Arg Gly Pro Gly Thr
202 145 150 155 160
205 Ser Phe Glu Phe Ala Leu Ala Ile Val Glu Ala Leu Ser Gly Lys Asp
206 165 170 175
209 Met Ala Asn Gln Val Lys Ala Pro Leu Val Leu Lys Asp
210 180 185
213 <210> SEQ ID NO: 4
214 <211> LENGTH: 57
215 <212> TYPE: DNA
216 <213> ORGANISM: Rattus rattus
218 <400> SEQUENCE: 4
219 tggcttcgcg tgggtggagg aggcgcggct gcaggtcttt aagaaataga aatggca

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57

**VERIFICATION SUMMARY**

**PATENT APPLICATION: US/09/752,514**

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